P8.1 Discrimination of *Xanthomonas campestris* pv. *campestris* races by means of Rep-PCR

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Xanthomonas campestris pv. *campestris* (Xcc), the bacterial causal agent of black rot, is widely distributed around the world in cultivated *Brassica* species, and is a major constraint on *Brassica* production. Based on avirulence/virulence patterns to six differential host genotypes, 9 races have been identified, which should been taken into account when searching for sources of resistance and to design adequate breeding programs. The established method to discriminate among races using differential series entails growing the host genotypes, inoculating them, and waiting until disease symptoms appear. It is therefore time consuming procedure. Repetitive DNA polymerase chain reaction-based fingerprinting (rep-PCR) is a rapid, low-cost, and reliable diagnostic method that has already been used to study genetic diversity within *Xanthomonas* and can be applied to identify the 9 existing Xcc races. DNA extraction and rep-PCR amplification were performed for type strains representing the nine races using REP, ERIC, and BOX primers. Strains were also classified into races using the differential series of *Brassica* spp. Based on DNA fingerprinting, BOX and ERIC primers discriminated 4 races each, and REP primers discriminated 3 races. Five out of 9 races could be discriminated with rep-PCR method. Race 1 could not be differentiated from race 7 and race 3 could not be differentiated from race 9, therefore more primers need to be added to the proposed method in order to discriminate between these pairs of races. Currently the reliability of the method is being checked by testing Xcc isolates collected in northwestern Spain and comparing the results using the differential series of *Brassica* spp.

Keywords: bacterial disease, black rot, Brassica crops, breeding, genetic fingerprinting, resistance